



#9

SEQUENCE LISTING

<110> Umezawa, Akihiro

Hata, Jun-Ichi

Fukuda, Keiichi

Ogawa, Satoshi

Sakurada, Kazuhiro

Gojo, Satoshi

Yamada, Yoji

<120> THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES

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<140> US/09/749,728

<141> 2001-09-17

<150> H11-372826

<151> 1999-12-28

<150> PCT-JP00-01148

<151> 2000-02-28

<150> PCT-JP00-07741

<151> 2000-11-02

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<170> PatentIn Ver.2.0

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Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln		
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275	280	285
Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu		
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Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr		
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Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile		
325	330	335
Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu		
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Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp		
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gag cag ggg ggc cag ggc agc gcg ctc gcc ccg tcc ccg gtg agc ggc 144
Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
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gtg cgc agg gaa ggc gct cgg ggc ggc ggc cgt ggc cgg ggg cgg tgg 192
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
          50          55          60
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Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
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Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
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Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
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Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
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Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
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gga ctt agt gca tca gat gta aca gaa caa att ata aaa acc atg gaa	912
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Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu	
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Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg	
50 55 60	
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ccc att cgg agg aag aga agc atc gag gaa gct gtc ccc gct gtc tgc	288
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys	
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aag acc agg acg gtc att tac gag att cct cgg agt cag gtc gac ccc	336
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro	
100 105 110	
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Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg	
115 120 125	
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Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg	
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Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
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Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
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Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg	
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Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp	
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Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val	
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Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg	

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gcc			723
Ala			

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 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
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 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
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 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt 288
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
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 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
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 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
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Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala				
	275	280	285	
aac aac aac ttc gtg aac ttc ggc gtc ggg gac ttg aat gcg gtt cag				912
Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln				
	290	295	300	
agc ccc ggg att ccg cag agc aac tcg gga gtg tcc acg ctg cat ggt				960
Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly				
305	310	315	320	
atc cga gcc tgg				972
Ile Arg Ala Trp				
	324			

<210> 11

<211> 442

<212> PRT

<213> Homo sapiens

<400> 11

Met Tyr Gln Ser Leu Ala Met Ala Ala Asn His Gly Pro Pro Pro Gly			
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Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala			
	20	25	30
Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val			
	35	40	45
Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly			
	50	55	60
Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro			
	65	70	75
Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly			
	85	90	95
Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly			
	100	105	110
Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu			
	115	120	125
Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala			
	130	135	140

Gly	Arg	Glu	Gln	Tyr	Gly	Arg	Ala	Gly	Phe	Ala	Gly	Ser	Tyr	Ser	Ser	
145					150				155						160	
Pro	Tyr	Pro	Ala	Tyr	Met	Ala	Asp	Val	Gly	Ala	Ser	Trp	Ala	Ala	Ala	
				165					170						175	
Ala	Ala	Ala	Ser	Ala	Gly	Pro	Phe	Asp	Ser	Pro	Val	Leu	His	Ser	Leu	
			180					185					190			
Pro	Gly	Arg	Ala	Asn	Pro	Ala	Ala	Arg	His	Pro	Asn	Leu	Asp	Met	Phe	
	195					200					205					
Asp	Asp	Phe	Ser	Glu	Gly	Arg	Glu	Cys	Val	Asn	Cys	Gly	Ala	Met	Ser	
	210					215					220					
Thr	Pro	Leu	Trp	Arg	Arg	Asp	Gly	Thr	Gly	His	Tyr	Leu	Cys	Asn	Ala	
225				230						235					240	
Cys	Gly	Leu	Tyr	His	Lys	Met	Asn	Gly	Ile	Asn	Arg	Pro	Leu	Ile	Lys	
				245					250						255	
Pro	Gln	Arg	Arg	Leu	Ser	Ala	Ser	Arg	Arg	Val	Gly	Leu	Ser	Cys	Ala	
				260				265					270			
Asn	Cys	Gln	Thr	Thr	Thr	Thr	Thr	Leu	Trp	Arg	Arg	Asn	Ala	Glu	Gly	
	275						280					285				
Glu	Pro	Val	Cys	Asn	Ala	Cys	Gly	Leu	Tyr	Met	Lys	Leu	His	Gly	Val	
	290					295				300						
Pro	Arg	Pro	Leu	Ala	Met	Arg	Lys	Glu	Gly	Ile	Gln	Thr	Arg	Lys	Arg	
305				310						315					320	
Lys	Pro	Lys	Asn	Leu	Asn	Lys	Ser	Lys	Thr	Pro	Ala	Ala	Pro	Ser	Gly	
			325					330					335			
Ser	Glu	Ser	Leu	Pro	Pro	Ala	Ser	Gly	Ala	Ser	Ser	Asn	Ser	Ser	Asn	
			340					345					350			
Ala	Thr	Thr	Ser	Ser	Ser	Glu	Glu	Met	Arg	Pro	Ile	Lys	Thr	Glu	Pro	
	355						360					365				
Gly	Leu	Ser	Ser	His	Tyr	Gly	His	Ser	Ser	Ser	Val	Ser	Gln	Thr	Phe	
	370					375					380					
Ser	Val	Ser	Ala	Met	Ser	Gly	His	Gly	Pro	Ser	Ile	His	Pro	Val	Leu	
385				390						395					400	
Ser	Ala	Leu	Lys	Leu	Ser	Pro	Gln	Gly	Tyr	Ala	Ser	Pro	Val	Ser	Gln	
			405					410					415			
Ser	Pro	Gln	Thr	Ser	Ser	Lys	Gln	Asp	Ser	Trp	Asn	Ser	Leu	Val	Leu	
		420						425					430			
Ala	Asp	Ser	His	Gly	Asp	Ile	Ile	Thr	Ala							
	435							440								

<210> 12

<211> 1326

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1329)

<400> 12

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gcc tac cag gcg ggc ggc ccc ggc ccc ttc atg cac ggc gcg ggc gcc	96
Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala	
20 25 30	
gcg tcc tcg cca gtc tac ctg ccc aca ccg cgg gtg ccc tcc' tcc gtt	144
Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val	
35 40 45	
ctg ggc ctg tcc tac ctg cag ggc gga ggc gcg ggc tct gcg tcc gga	192
Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly	
50 55 60	
ggc ccc tcg ggc ggc agc ccc ggt ggg gcc gcg tct ggt gcg ggg ccc	240
Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro	
65 70 75 80	
ggg acc cag cag ggc agc ccg gga tgg agc cag gcg gga gcg acc gga	288
Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly	
85 90 95	
gcc gct tac acc ccg ccg ccg gtg tcg ccg cgc ttc tcc ttc ccg ggg	336
Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly	
100 105 110	
acc acc ggg tcc ctg gcg gcg gcg gcg gcg gct gcc gcc gcc ccg gaa	384
Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu	
115 120 125	
gct gcg gcc tac agc agt ggc ggc gga gcg gcg ggt gcg ggc ctg gcg	432
Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala	
130 135 140	
ggc cgc gag cag tac ggg cgc gcc ggc ttc gcg ggc tcc tac tcc agc	480
Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser	
145 150 155 160	
ccc tac ccg gct tac atg gcc gac gtg ggc gcg tcc tgg gcc gca gcc	528
Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala	
165 170 175	
gcc gcc gcc tcc gcc ggc ccc ttc gac agc ccg gtc ctg cac agc ctg	576
Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu	
180 185 190	
ccc ggc cgg gcc aac ccg gcc gcc cga cac ccc aat ctg gat atg ttt	624
Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Asp Met Phe	

195	200	205	
gac gac ttc tca gaa ggc aga gag tgt gtc aac tgt ggg gct atg tcc	672		
Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met Ser			
210	215	220	
acc ccg ctc tgg agg cga gat ggg acg ggt cac tat ctg tgc aac gcc	720		
Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala			
225	230	235	240
tgt ggc ctc tac cac aag atg aac ggc atc aac cgg ccg ctc atc aag	768		
Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile Lys			
245	250	255	
cct cag cgc cgg ctg tcc gcc tcc cgc cga gtg ggc ctc tcc tgt gcc	816		
Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys Ala			
260	265	270	
aac tgc cag acc acc acc acc acg ctg tgg cgc cgc aat gcg gag ggc	864		
Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu Gly			
275	280	285	
gag cct gtg tgc aat gcc tgc ggc ctc tac atg aag ctc cac ggg gtg	912		
Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly Val			
290	295	300	
ccc agg cct ctt gca atg cgg aaa gag ggg atc caa acc aga aaa cgg	960		
Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys Arg			
305	310	315	320
aag ccc aag aac ctg aat aaa tct aag aca cca gca gct cct tca ggc	1008		
Lys Pro Lys Asn Leu Asn Lys Ser Lys Thr Pro Ala Ala Pro Ser Gly			
325	330	335	
agt gag agc ctt cct ccc gcc agc ggt gct tcc agc aac tcc agc aac	1056		
Ser Glu Ser Leu Pro Pro Ala Ser Gly Ala Ser Ser Asn Ser Ser Asn			
340	345	350	
gcc acc acc agc agc agc gag gag atg cgt ccc atc aag acg gag cct	1104		
Ala Thr Thr Ser Ser Ser Glu Glu Met Arg Pro Ile Lys Thr Glu Pro			
355	360	365	
ggc ctg tca tct cac tac ggg cac agc agc tcc gtg tcc cag acg ttc	1152		
Gly Leu Ser Ser His Tyr Gly His Ser Ser Ser Val Ser Gln Thr Phe			
370	375	380	
tca gtc agt gcg atg tct ggc cat ggg ccc tcc atc cac cct gtc ctc	1200		
Ser Val Ser Ala Met Ser Gly His Gly Pro Ser Ile His Pro Val Leu			
385	390	395	400
tcg gcc ctg aag ctc tcc cca caa ggc tat gcg tct ccc gtc agc cag	1248		
Ser Ala Leu Lys Leu Ser Pro Gln Gly Tyr Ala Ser Pro Val Ser Gln			
405	410	415	
tct cca cag acc agc tcc aag cag gac tct tgg aac agt ctg gtc ttg	1296		
Ser Pro Gln Thr Ser Ser Lys Gln Asp Ser Trp Asn Ser Leu Val Leu			

420 425 430 1326
 gcc gac agt cac ggg gac ata atc act gcg
 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
 435 440
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 <211> 507
 <212> PRT
 <213> Homo sapiens
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 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
 100 105 110
 Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
 115 120 125
 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
 130 135 140
 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
 145 150 155 160
 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
 165 170 175
 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
 180 185 190
 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
 195 200 205
 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
 210 215 220
 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
 225 230 235 240
 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
 245 250 255
 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp

260	265	270
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu		
275	280	285
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser		
290	295	300
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro		
305	310	315
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr		
325	330	335
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly		
340	345	350
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln		
355	360	365
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly		
370	375	380
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile		
385	390	395
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro		
405	410	415
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro		
420	425	430
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln		
435	440	445
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser		
450	455	460
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro		
465	470	475
Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser		
485	490	495
Val Lys Arg Met Arg Met Asp Ala Trp Val Thr		
500	505	

<210> 14

<211> 1521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1524)

<400> 14

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Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn

1

5

10

15

cga cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa	192
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys	
50 55 60	
gtt ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc	240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac tgc gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc	288
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys	
85 90 95	
gac agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa	336
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu	
100 105 110	
gaa aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat	384
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn	
115 120 125	
cat aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc	432
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val	
130 135 140	
aca gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg	480
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly	
145 150 155 160	
agt tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat	528
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp	
165 170 175	
tca agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct	576
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser	
180 185 190	
cct gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg	624
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met	
195 200 205	
ttg agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca	672
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro	
210 215 220	
gtg ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga	720
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly	
225 230 235 240	

gct act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc	768
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro	
245 250 255	
cct cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat	816
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp	
260 265 270	
ctt cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta	864
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu	
275 280 285	
tcg gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct	912
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser	
290 295 300	
caa gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca	960
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro	
305 310 315 320	
agc ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac	1008
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr	
325 330 335	
aac act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc	1056
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly	
340 345 350	
ttc aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag	1104
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln	
355 360 365	
cag cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg	1152
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly	
370 375 380	
cag tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc	1200
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile	
385 390 395 400	
agc atc aag tcc gaa ccg att tca cct cct ccg gat cgt atg acc cca	1248
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro	
405 410 415	
tcg ggc ttc cag cag cag cag cag cag cag cag cag cag ccg ccg	1296
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro	
420 425 430	
cca cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag	1344
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln	
435 440 445	
gaa atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc	1392
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser	
450 455 460	

tat	gat	ggc	agt	gat	cgg	gag	gat	cca	cgg	ggc	gac	ttc	cat	tct	cca	1440
Tyr	Asp	Gly	Ser	Asp	Arg	Glu	Asp	Pro	Arg	Gly	Asp	Phe	His	Ser	Pro	
465					470					475					480	
att	gtg	ctt	ggc	cga	ccc	cca	aac	act	gag	gac	aga	gaa	agc	cct	tct	1488
Ile	Val	Leu	Gly	Arg	Pro	Pro	Asn	Thr	Glu	Asp	Arg	Glu	Ser	Pro	Ser	
				485						490				495		
gta	aag	cga	atg	agg	atg	gac	gcg	tgg	gtg	acc						1521
Val	Lys	Arg	Met	Arg	Met	Asp	Ala	Trp	Val	Thr						
			500					505								

<210> 15

<211> 365

<212> PRT

<213> Homo sapiens

<400> 15

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			20					25					30		
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe
		35					40					45			
Asn	Ser	Ala	Asn	Arg	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Arg
	50					55				60					
Val	Leu	Leu	Lys	Tyr	Thr	Glu	Tyr	Ser	Glu	Pro	His	Glu	Ser	Arg	Thr
65				70					75					80	
Asn	Thr	Asp	Ile	Leu	Glu	Thr	Leu	Lys	Arg	Arg	Gly	Ile	Gly	Leu	Asp
			85					90					95		
Gly	Pro	Glu	Leu	Glu	Pro	Asp	Glu	Gly	Pro	Glu	Glu	Pro	Gly	Glu	Lys
			100				105					110			
Phe	Arg	Arg	Leu	Ala	Gly	Glu	Gly	Gly	Asp	Pro	Ala	Leu	Pro	Arg	Pro
		115				120					125				
Arg	Leu	Tyr	Pro	Ala	Ala	Pro	Ala	Met	Pro	Ser	Pro	Asp	Val	Val	Tyr
	130					135				140					
Gly	Ala	Leu	Pro	Pro	Pro	Gly	Cys	Asp	Pro	Ser	Gly	Leu	Gly	Glu	Ala
145				150					155					160	
Leu	Pro	Ala	Gln	Ser	Arg	Pro	Ser	Pro	Phe	Arg	Pro	Ala	Ala	Pro	Lys
			165					170				175			
Ala	Gly	Pro	Pro	Gly	Leu	Val	His	Pro	Leu	Phe	Ser	Pro	Ser	His	Leu
		180				185					190				
Thr	Ser	Lys	Thr	Pro	Pro	Pro	Leu	Tyr	Leu	Pro	Thr	Glu	Gly	Arg	Arg
		195				200					205				
Ser	Asp	Leu	Pro	Gly	Gly	Leu	Ala	Gly	Pro	Arg	Gly	Gly	Leu	Asn	Thr
	210					215				220					

Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
 225 230 235 240
 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
 245 250 255
 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
 260 265 270
 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
 275 280 285
 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
 290 295 300
 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
 305 310 315 320
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
 340 345 350
 Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
 355 360

<210> 16

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1098)

<400> 16

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 cgg cag gtg acg ttc acc aag cgg aag ttc ggg ctg atg aag aag gcc 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gag ctg agc gtg ctc tgt gac tgt gag ata gcc ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac agc gcc aac cgc ctc ttc cag tat gcc agc acg gac atg gac cgt 192
 Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
 50 55 60
 gtg ctg ctg aag tac aca gag tac agc gag ccc cac gag agc cgc acc 240
 Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 aac act gac atc ctc gag acg ctg aag cgg agg ggc att ggc ctc gat 288

Asn	Thr	Asp	Ile	Leu	Glu	Thr	Leu	Lys	Arg	Arg	Gly	Ile	Gly	Leu	Asp		
				85					90					95			
ggg	cca	gag	ctg	gag	ccg	gat	gaa	ggg	cct	gag	gag	cca	gga	gag	aag	336	
Gly	Pro	Glu	Leu	Glu	Pro	Asp	Glu	Gly	Pro	Glu	Glu	Pro	Gly	Glu	Lys		
			100					105					110				
ttt	cgg	agg	ctg	gca	ggc	gaa	ggg	ggt	gat	ccg	gcc	ttg	ccc	cga	ccc	384	
Phe	Arg	Arg	Leu	Ala	Gly	Glu	Gly	Gly	Asp	Pro	Ala	Leu	Pro	Arg	Pro		
			115				120					125					
cgg	ctg	tat	cct	gca	gct	cct	gct	atg	ccc	agc	cca	gat	gtg	gta	tac	432	
Arg	Leu	Tyr	Pro	Ala	Ala	Pro	Ala	Met	Pro	Ser	Pro	Asp	Val	Val	Tyr		
			130				135					140					
ggg	gcc	tta	ccg	cca	cca	ggc	tgt	gac	ccc	agt	ggg	ctt	ggg	gaa	gca	480	
Gly	Ala	Leu	Pro	Pro	Pro	Gly	Cys	Asp	Pro	Ser	Gly	Leu	Gly	Glu	Ala		
			145			150			155					160			
ctg	ccc	gcc	cag	agc	cgc	cca	tct	ccc	ttc	cga	cca	gca	gcc	ccc	aaa	528	
Leu	Pro	Ala	Gln	Ser	Arg	Pro	Ser	Pro	Phe	Arg	Pro	Ala	Ala	Pro	Lys		
			165					170					175				
gcc	ggg	ccc	cca	ggc	ctg	gtg	cac	cct	ctc	ttc	tca	cca	agc	cac	ctc	576	
Ala	Gly	Pro	Pro	Gly	Leu	Val	His	Pro	Leu	Phe	Ser	Pro	Ser	His	Leu		
			180					185					190				
acc	agc	aag	aca	cca	ccc	cca	ctg	tac	ctg	ccg	acg	gaa	ggg	cgg	agg	624	
Thr	Ser	Lys	Thr	Pro	Pro	Pro	Leu	Tyr	Leu	Pro	Thr	Glu	Gly	Arg	Arg		
			195				200					205					
tca	gac	ctg	cct	ggt	ggc	ctg	gct	ggg	ccc	cga	ggg	gga	cta	aac	acc	672	
Ser	Asp	Leu	Pro	Gly	Gly	Leu	Ala	Gly	Pro	Arg	Gly	Gly	Leu	Asn	Thr		
			210			215					220						
tcc	aga	agc	ctc	tac	agt	ggc	ctg	cag	aac	ccc	tgc	tcc	act	gca	act	720	
Ser	Arg	Ser	Leu	Tyr	Ser	Gly	Leu	Gln	Asn	Pro	Cys	Ser	Thr	Ala	Thr		
			225			230				235			240				
ccc	gga	ccc	cca	ctg	ggg	agc	ttc	ccc	ttc	ctc	ccc	gga	ggc	ccc	cca	768	
Pro	Gly	Pro	Pro	Leu	Gly	Ser	Phe	Pro	Phe	Leu	Pro	Gly	Gly	Pro	Pro		
			245					250					255				
gtg	ggg	gcc	gaa	gcc	tgg	gcg	agg	agg	gtc	ccc	caa	ccc	gcg	gcg	cct	816	
Val	Gly	Ala	Glu	Ala	Trp	Ala	Arg	Arg	Val	Pro	Gln	Pro	Ala	Ala	Pro		
			260					265					270				
ccc	cgc	cga	ccc	ccc	cag	tca	gca	tca	agt	ctg	agc	gcc	tct	ctc	cgg	864	
Pro	Arg	Arg	Pro	Pro	Gln	Ser	Ala	Ser	Ser	Leu	Ser	Ala	Ser	Leu	Arg		
			275				280					285					
ccc	ccg	ggg	gcc	ccg	gcg	act	ttc	cta	aga	cct	tcc	cct	atc	cct	tgc	912	
Pro	Pro	Gly	Ala	Pro	Ala	Thr	Phe	Leu	Arg	Pro	Ser	Pro	Ile	Pro	Cys		
			290				295					300					
tcc	tgc	ccc	ggt	ccc	tgg	cag	agc	ctc	tgc	ggc	ctg	ggc	ccg	ccc	tgc	960	

Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
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 gcc gcc tgc cct tgg ccg acg gct ggc ccc ggt agg aga tca ccc ggt 1008
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 ggc acc agc cca gag cgc tcg cca ggt acg gcg agg gca cgt ggg gac 1056
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
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 ccc acc tcc ctc cag gcc tct tca gag aag acc caa cag 1095
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 <213> Homo sapiens
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 35 40 45
 Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
 100 105 110
 Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
 115 120 125
 Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
 130 135 140
 Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
 145 150 155 160
 Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
 165 170 175
 Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
 180 185 190
 Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
 195 200 205

Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
 210 215 220
 Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
 225 230 235 240
 Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg
 245 250 255
 Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln
 260 265 270
 Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val
 275 280 285
 Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro
 290 295 300
 Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala
 305 310 315 320
 Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu
 325 330 335
 Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro
 340 345 350
 Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln
 355 360 365
 Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser
 370 375 380
 Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr
 385 390 395 400
 Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu
 405 410 415
 Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg
 420 425 430
 Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu
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 Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala
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Thr

<210> 18

<211> 1395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1398)

<400> 18

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aga	cag	gtg	aca	ttt	aca	aag	agg	aaa	ttt	ggg	ttg	atg	aag	aag	gct	96
Arg	Gln	Val	Thr	Phe	Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala	
			20					25					30			
tat	gag	ctg	agc	gtg	ctg	tgt	gac	tgt	gag	att	gcg	ctg	atc	atc	ttc	144
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe	
		35					40					45				
aac	agc	acc	aac	aag	ctg	ttc	cag	tat	gcc	agc	acc	gac	atg	gac	aaa	192
Asn	Ser	Thr	Asn	Lys	Leu	Phe	Gln	Tyr	Ala	Ser	Thr	Asp	Met	Asp	Lys	
		50					55				60					
gtg	ctt	ctc	aag	tac	acg	gag	tac	aac	gag	ccg	cat	gag	agc	cgg	aca	240
Val	Leu	Leu	Lys	Tyr	Thr	Glu	Tyr	Asn	Glu	Pro	His	Glu	Ser	Arg	Thr	
	65					70				75				80		
aac	tca	gac	atc	gtg	gag	acg	ttg	aga	aag	aag	ggc	ctt	aat	ggc	tgt	288
Asn	Ser	Asp	Ile	Val	Glu	Thr	Leu	Arg	Lys	Lys	Gly	Leu	Asn	Gly	Cys	
			85					90			95					
gac	agc	cca	gac	ccc	gat	gcg	gac	gat	tcc	gta	ggc	cac	agc	cct	gag	336
Asp	Ser	Pro	Asp	Pro	Asp	Ala	Asp	Asp	Ser	Val	Gly	His	Ser	Pro	Glu	
		100						105				110				
tct	gag	gac	aag	tac	agg	aaa	att	aac	gaa	gat	att	gat	cta	atg	atc	384
Ser	Glu	Asp	Lys	Tyr	Arg	Lys	Ile	Asn	Glu	Asp	Ile	Asp	Leu	Met	Ile	
		115					120				125					
agc	agg	caa	aga	ttg	tgt	gct	gtt	cca	cct	ccc	aac	ttc	gag	atg	cca	432
Ser	Arg	Gln	Arg	Leu	Cys	Ala	Val	Pro	Pro	Pro	Asn	Phe	Glu	Met	Pro	
	130					135				140						
gtc	tcc	atc	cca	gtg	tcc	agc	cac	aac	agt	ttg	gtg	tac	agc	aac	cct	480
Val	Ser	Ile	Pro	Val	Ser	Ser	His	Asn	Ser	Leu	Val	Tyr	Ser	Asn	Pro	
	145				150					155				160		
gtc	agc	tca	ctg	gga	aac	ccc	aac	cta	ttg	cca	ctg	gct	cac	cct	tct	528
Val	Ser	Ser	Leu	Gly	Asn	Pro	Asn	Leu	Leu	Pro	Leu	Ala	His	Pro	Ser	
			165					170				175				
ctg	cag	agg	aat	agt	atg	tct	cct	ggc	gta	aca	cat	cga	cct	cca	agt	576
Leu	Gln	Arg	Asn	Ser	Met	Ser	Pro	Gly	Val	Thr	His	Arg	Pro	Pro	Ser	
		180						185				190				
gca	ggc	aac	aca	ggc	ggc	ctg	atg	ggc	gga	gac	ctc	acg	tct	ggc	gca	624
Ala	Gly	Asn	Thr	Gly	Gly	Leu	Met	Gly	Gly	Asp	Leu	Thr	Ser	Gly	Ala	
		195					200				205					
ggc	acc	agt	gca	ggg	aac	ggg	tat	ggc	aat	ccc	cga	aac	tca	cca	ggc	672
Gly	Thr	Ser	Ala	Gly	Asn	Gly	Tyr	Gly	Asn	Pro	Arg	Asn	Ser	Pro	Gly	
	210					215					220					
ctg	ctg	gtc	tca	cct	ggc	aac	ttg	aac	aag	aat	atg	caa	gca	aaa	tct	720

Leu	Leu	Val	Ser	Pro	Gly	Asn	Leu	Asn	Lys	Asn	Met	Gln	Ala	Lys	Ser		
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Pro	Pro	Pro	Met	Asn	Leu	Gly	Met	Asn	Asn	Arg	Lys	Pro	Asp	Leu	Arg		
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gtt	ctt	att	cca	cca	ggc	agc	aag	aat	acg	atg	cca	tca	gtg	aat	caa	816	
Val	Leu	Ile	Pro	Pro	Gly	Ser	Lys	Asn	Thr	Met	Pro	Ser	Val	Asn	Gln		
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agg	ata	aat	aac	tcc	cag	tcg	gct	cag	tca	ttg	gct	acc	cca	gtg	gtt	864	
Arg	Ile	Asn	Asn	Ser	Gln	Ser	Ala	Gln	Ser	Leu	Ala	Thr	Pro	Val	Val		
		275						280					285				
tcc	gta	gca	act	cct	act	tta	cca	gga	caa	gga	atg	gga	gga	tat	cca	912	
Ser	Val	Ala	Thr	Pro	Thr	Leu	Pro	Gly	Gln	Gly	Met	Gly	Gly	Tyr	Pro		
		290						295					300				
tca	gcc	att	tca	aca	aca	tat	ggg	acc	gag	tac	tct	ctg	agt	agt	gca	960	
Ser	Ala	Ile	Ser	Thr	Thr	Tyr	Gly	Thr	Glu	Tyr	Ser	Leu	Ser	Ser	Ala		
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gac	ctg	tca	tct	ctg	tct	ggg	ttt	aac	acc	gcc	agc	gct	ctt	cac	ctt	1008	
Asp	Leu	Ser	Ser	Leu	Ser	Gly	Phe	Asn	Thr	Ala	Ser	Ala	Leu	His	Leu		
				325					330					335			
ggg	tca	gta	act	ggc	tgg	caa	cag	caa	cac	cta	cat	aac	atg	cca	cca	1056	
Gly	Ser	Val	Thr	Gly	Trp	Gln	Gln	Gln	His	Leu	His	Asn	Met	Pro	Pro		
				340					345					350			
tct	gcc	ctc	agt	cag	ttg	gga	gct	tgc	act	agc	act	cat	tta	tct	cag	1104	
Ser	Ala	Leu	Ser	Gln	Leu	Gly	Ala	Cys	Thr	Ser	Thr	His	Leu	Ser	Gln		
		355						360					365				
agt	tca	aat	ctc	tcc	ctg	cct	tct	act	caa	agc	ctc	aac	atc	aag	tca	1152	
Ser	Ser	Asn	Leu	Ser	Leu	Pro	Ser	Thr	Gln	Ser	Leu	Asn	Ile	Lys	Ser		
		370					375					380					
gaa	cct	gtt	tct	cct	cct	aga	gac	cgt	acc	acc	acc	cct	tcg	aga	tac	1200	
Glu	Pro	Val	Ser	Pro	Pro	Arg	Asp	Arg	Thr	Thr	Thr	Pro	Ser	Arg	Tyr		
385					390					395				400			
cca	caa	cac	acg	cgc	cac	gag	gcg	ggg	aga	tct	cct	gtt	gac	agc	ttg	1248	
Pro	Gln	His	Thr	Arg	His	Glu	Ala	Gly	Arg	Ser	Pro	Val	Asp	Ser	Leu		
				405					410					415			
agc	agc	tgt	agc	agt	tcg	tac	gac	ggg	agc	gac	cga	gag	gat	cac	cgg	1296	
Ser	Ser	Cys	Ser	Ser	Ser	Tyr	Asp	Gly	Ser	Asp	Arg	Glu	Asp	His	Arg		
		420						425					430				
aac	gaa	ttc	cac	tcc	ccc	att	gga	ctc	acc	aga	cct	tcg	ccg	gac	gaa	1344	
Asn	Glu	Phe	His	Ser	Pro	Ile	Gly	Leu	Thr	Arg	Pro	Ser	Pro	Asp	Glu		
		435						440					445				
agg	gaa	agt	ccc	tca	gtc	aag	cgc	atg	cga	ctt	tct	gaa	gga	tgg	gca	1392	

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aca 1395

Thr

465

<210> 19

<211> 521

<212> PRT

<213> Homo sapiens

<400> 19

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 20 25 30

Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45

Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60

Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80

Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys
 85 90 95

Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu
 100 105 110

Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe
 115 120 125

Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val
 130 135 140

Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser
 145 150 155 160

Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro
 165 170 175

Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser
 180 185 190

Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly
 195 200 205

Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly
 210 215 220

Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly
 225 230 235 240

Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr
 245 250 255

His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val			
260	265	270	
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp			
275	280	285	
His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr			
290	295	300	
His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu			
305	310	315	320
Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp			
325	330	335	
Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser			
340	345	350	
Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln			
355	360	365	
Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro			
370	375	380	
Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro			
385	390	395	400
Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile			
405	410	415	
Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr			
420	425	430	
His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu			
435	440	445	
Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro			
450	455	460	
Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr			
465	470	475	480
Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu			
485	490	495	
Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg			
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Met Arg Leu Asp Thr Trp Thr Leu Lys			
515	520		

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<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1566)

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cga cag gtg act ttc acc aag cgg aag ttt ggc ctg atg aag aag gcg	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
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tat gag ctg agc gtg cta tgt gac tgc gag atc gca ctc atc atc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac cac tcc aac aag ctg ttc cag tac gcc agc acc gac atg gac aag	192
Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys	
50 55 60	
gtg ctg ctc aag tac acg gag tac aat gag cca cac gag agc cgc acc	240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac gcc gac atc atc gag acc ctg agg aag aag ggc ttc aat ggc tgc	288
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys	
85 90 95	
gac agc ccc gag ccc gac ggg gag gac tcg ctg gaa cag agc ccc ctg	336
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu	
100 105 110	
ctg gag gac aag tac cga cgc gcc agc gag gag ctc gac ggg ctc ttc	384
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe	
115 120 125	
cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt gcc atg cct gtc	432
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val	
130 135 140	
acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc agc aat ccc agc	480
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser	
145 150 155 160	
ggc tcc ctg gtc acc cct tcc ctg gtg aca tca tcc ctc acg gac ccg	528
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro	
165 170 175	
cgg ctc ctg tcc ccc cag cag cca gca cta cag agg aac agt gtg tct	576
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser	
180 185 190	
cct ggc ctg ccc cag cgg cca gct agt gcg ggg gcc atg ctg ggg ggt	624
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly	
195 200 205	
gac ctg aac agt gct aac gga gcc tgc ccc agc cct gtt ggg aat ggc	672
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly	
210 215 220	

cgc agc cct gcg cct ccc cct cca gct gtg ttc cca gct gcc cgc cct 1392
 Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro
 450 455 460
 gag cct ggc gat ggt ctc agc agc cca gcc ggg gga tcc tat gag acg 1440
 Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr
 465 470 475 480
 gga gac cgg gat gac gga cgg ggg gac ttc ggg ccc aca ctg ggc ctg 1488
 Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu
 485 490 495
 ctg cgc cca gcc cca gag cct gag gct gag ggc tca gct gtg aag agg 1536
 Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg
 500 505 510
 atg cgg ctt gat acc tgg aca tta aag 1563
 Met Arg Leu Asp Thr Trp Thr Leu Lys
 515 520
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 <211> 217
 <212> PRT
 <213> Rattus norvegicus
 <400> 21
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 Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
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 Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile
 35 40 45
 Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr
 50 55 60
 Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr
 65 70 75 80
 Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg
 85 90 95
 Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr
 100 105 110
 Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn
 115 120 125
 Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala
 130 135 140
 Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
 145 150 155 160
 Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
 165 170 175

Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
180 185 190
Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
195 200 205
His Val Trp Ala Leu Glu Leu Lys Gln
210 215

<210> 22

<211> 651

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<223> (1)..(654)

<400> 22

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ggc tac ccg ttc gcc gca gcc gca gcc gcc gct gct gct gcc gcc gcc	96
Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala	
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agc cgc tgc agt cac gag gag aac ccc tat ttc cac ggc tgg ctt att	144
Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile	
35 40 45	
ggc cac ccg gag atg tcg ccc ccc gac tac agc atg gcc ctg tcc tac	192
Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr	
50 55 60	
agt ccc gag tac gcc agc ggt gcc gcg ggc ctg gac cac tcc cat tat	240
Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr	
65 70 75 80	
ggg gga gtg ccg ccc ggt gcc ggg cct ccc ggc ctg ggg ggg ccg cgc	288
Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg	
85 90 95	
ccg gtg aag cgt cgg ggc acc gcc aac cgc aag gag cgg cgc agg act	336
Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr	
100 105 110	
cag agc atc aac agc gcc ttc gcc gag ctg cgc gag tgc atc ccc aac	384
Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn	
115 120 125	
gtg ccc gcc gac acc aaa ctc tcc aaa atc aag act ctg cgc ctg gcc	432
Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala	
130 135 140	
acc agc tac atc gcc tac ctc atg gat ctg ctg gcc aag gac gac cag	480

Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
 145 150 155 160
 aac gga gag gcg gag gcc ttc aag gcg gag atc aag aag acc gac gtg 528
 Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
 165 170 175
 aaa gag gag aag agg aag aaa gag ctg aat gaa atc ttg aaa agt aca 576
 Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
 180 185 190
 gtg agc agc aac gac aag aaa acc aaa ggc cgg aca ggc tgg cca cag 624
 Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
 195 200 205
 cac gtc tgg gcc ctg gag ctc aag cag 651
 His Val Trp Ala Leu Glu Leu Lys Gln
 210 215
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 Met Asn Leu Val Gly Ser Tyr Ala His His His His His His Pro
 1 5 10 15
 His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
 20 25 30
 Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45
 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60
 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80
 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95
 Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
 100 105 110
 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
 115 120 125
 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
 130 135 140
 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
 145 150 155 160
 Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
 165 170 175
 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly

180	185	190	
Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp	Pro Gln Gln Val		
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Trp Ala Leu Glu Leu Asn Gln			
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Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro			
1 5 10 15			
cac cct gcg cac ccc atg ctc cac gaa ccc ttc ctc ttc ggt ccg gcc	96		
His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala			
20 25 30			
tcg cgc tgt cat cag gaa agg ccc tac ttc cag agc tgg ctg ctg agc	144		
Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser			
35 40 45			
ccg gct gac gct gcc ccg gac ttc cct gcg ggc ggg ccg ccg ccc gcg	192		
Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala			
50 55 60			
gcc gct gca gcc gcc acc gcc tat ggt cct gac gcc agg cct ggg cag	240		
Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln			
65 70 75 80			
agc ccc ggg cgg ctg gag gcg ctt ggc ggc cgt ctt ggc cgg cgg aaa	288		
Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys			
85 90 95			
ggc tca gga ccc aag aag gag cgg aga cgc act gag agc att aac agc	336		
Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser			
100 105 110			
gca ttc gcg gag ttg cgc gag tgc atc ccc aac gtg ccg gcc gac acc	384		
Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr			
115 120 125			
aag ctc tcc aag atc aag act ctg cgc cta gcc acc agc tac atc gcc	432		
Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala			
130 135 140			
tac ctg atg gac gtg ctg gcc aag gat gca cag tct ggc gat ccc gag	480		
Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu			

145	150	155	160	
gcc ttc aag gct gaa ctc aag aag gcg gat ggc ggc cgt gag agc aag	528			
Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys				
165	170	175		
cgg aaa agg gag ctg cag cag cac gaa ggt ttt cct cct gcc ctg ggc	576			
Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly				
180	185	190		
cca gtc gag aag agg att aaa gga cgc acc ggc tgg ccg cag caa gtc	624			
Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val				
195	200	205		
tgg gcg ctg gag tta aac cag	645			
Trp Ala Leu Glu Leu Asn Gln				
210	215			
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Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu				
20 25 30				
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu				
35 40 45				
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu				
50 55 60				
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln				
65 70 75 80				
Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp				
85 90 95				
Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser				
100 105 110				
Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro				
115 120 125				
Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly				
130 135 140				
Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe				
145 150 155 160				
Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro				
165 170 175				
Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln				
180 185 190				

Gly	Arg	Ser	Ile	Gly	Thr	Thr	Lys	Leu	Arg	Leu	Val	Glu	Phe	Ser	Ala
195				200				205							
Phe	Leu	Glu	Gln	Gln	Arg	Asp	Pro	Asp	Ser	Tyr	Asn	Lys	His	Leu	Phe
210				215				220							
Val	His	Ile	Gly	His	Ala	Asn	His	Ser	Tyr	Ser	Asp	Pro	Leu	Leu	Glu
225				230				235				240			
Ser	Val	Asp	Ile	Arg	Gln	Ile	Tyr	Asp	Lys	Phe	Pro	Glu	Lys	Lys	Gly
245				250				255							
Gly	Leu	Lys	Glu	Leu	Phe	Gly	Lys	Gly	Pro	Gln	Asn	Ala	Phe	Phe	Leu
260				265				270							
Val	Lys	Phe	Trp	Ala	Asp	Leu	Asn	Cys	Asn	Ile	Gln	Asp	Asp	Ala	Gly
275				280				285							
Ala	Phe	Tyr	Gly	Val	Thr	Ser	Gln	Tyr	Glu	Ser	Ser	Glu	Asn	Met	Thr
290				295				300							
Val	Thr	Cys	Ser	Thr	Lys	Val	Cys	Ser	Phe	Gly	Lys	Gln	Val	Val	Glu
305				310				315				320			
Lys	Val	Glu	Thr	Glu	Tyr	Ala	Arg	Phe	Glu	Asn	Gly	Arg	Phe	Val	Tyr
325				330				335							
Arg	Ile	Asn	Arg	Ser	Pro	Met	Cys	Glu	Tyr	Met	Ile	Asn	Phe	Ile	His
340				345				350							
Lys	Leu	Lys	His	Leu	Pro	Glu	Lys	Tyr	Met	Met	Asn	Ser	Val	Leu	Glu
355				360				365							
Asn	Phe	Thr	Ile	Leu	Leu	Val	Val	Thr	Asn	Arg	Asp	Thr	Gln	Glu	Thr
370				375				380							
Leu	Leu	Cys	Met	Ala	Cys	Val	Phe	Glu	Val	Ser	Asn	Ser	Glu	His	Gly
385				390				395				400			
Ala	Gln	His	His	Ile	Tyr	Arg	Leu	Val	Lys	Asp					
405				410											

<210> 26

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

<400> 26

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Met	Glu	Arg	Met	Ser	Asp	Ser	Ala	Asp	Lys	Pro	Ile	Asp	Asn	Asp	Ala	
1	5				10				15							
gaa	ggg	gtc	tgg	agc	ccc	gac	atc	gag	caa	agc	ttt	cag	gag	gcc	ctg	96
Glu	Gly	Val	Trp	Ser	Pro	Asp	Ile	Glu	Gln	Ser	Phe	Gln	Glu	Ala	Leu	
20				25				30								

gct atc tat cca cca tgt ggg agg agg aaa atc atc tta tca gac gaa	144
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu	
35 40 45	
ggc aaa atg tat ggt agg aat gaa ttg ata gcc aga tac atc aaa ctc	192
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu	
50 55 60	
agg aca ggc aag acg agg acc aga aaa cag gtg tct agt cac att cag	240
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln	
65 70 75 80	
gtt ctt gcc aga agg aaa tct cgt gat ttt cat tcc aag cta aag gat	288
Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp	
85 90 95	
cag act gca aag gat aag gcc ctg cag cac atg gcg gcc atg tcc tca	336
Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser	
100 105 110	
gcc cag atc gtc tcg gcc act gcc att cat aac aag ctg ggg ctg cct	384
Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro	
115 120 125	
ggg att cca cgc ccg acc ttc cca ggg gcg ccg ggg ttc tgg ccg gga	432
Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly	
130 135 140	
atg att caa aca ggg cag cca gga tcc tca caa gac gtc aag cct ttt	480
Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe	
145 150 155 160	
gtg cag cag gcc tac ccc atc cag cca gcg gtc aca gcc ccc att cca	528
Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro	
165 170 175	
ggg ttt gag cct gca tcg gcc cca gct ccc tca gtc cct gcc tgg caa	576
Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln	
180 185 190	
ggt cgc tcc att ggc aca acc aag ctt cgc ctg gtg gaa ttt tca gct	624
Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala	
195 200 205	
ttt ctc gag cag cag cga gac cca gac tcg tac aac aaa cac ctc ttc	672
Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe	
210 215 220	
gtg cac att ggg cat gcc aac cat tct tac agt gac cca ttg ctt gaa	720
Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu	
225 230 235 240	
tca gtg gac att cgt cag att tat gac aaa ttt cct gaa aag aaa ggt	768
Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly	
245 250 255	

ggc tta aag gaa ctg ttt gga aag ggc cct caa aat gcc ttc ttc ctc 816
 Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu
 260 265 270
 gta aaa ttc tgg gct gat tta aac tgc aat att caa gat gat gct ggg 864
 Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly
 275 280 285
 gct ttt tat ggt gta acc agt cag tac gag agt tct gaa aat atg aca 912
 Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr
 290 295 300
 gtc acc tgt tcc acc aaa gtt tgc tcc ttt ggg aag caa gta gta gaa 960
 Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
 305 310 315 320
 aaa gta gag acg gag tat gca agg ttt gag aat ggc cga ttt gta tac 1008
 Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr
 325 330 335
 cga ata aac cgc tcc cca atg tgt gaa tat atg atc aac ttc atc cac 1056
 Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His
 340 345 350
 aag ctc aaa cac tta cca gag aaa tat atg atg aac agt gtt ttg gaa 1104
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 355 360 365
 aac ttc aca att tta ttg gtg gta aca aac agg gat aca caa gaa act 1152
 Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 370 375 380
 cta ctc tgc atg gcc tgt gtg ttt gaa gtt tca aat agt gaa cac gga 1200
 Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly
 385 390 395 400
 gca caa cat cat att tac agg ctt gta aag gac 1233
 Ala Gln His His Ile Tyr Arg Leu Val Lys Asp
 405 410

<210> 27

<211> 427

<212> PRT

<213> Homo sapiens

<400> 27

Ile Thr Ser Asn Glu Trp Ser Ser Pro Thr Ser Pro Glu Gly Ser Thr
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 20 25 30
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu
 35 40 45
 Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu

50	55	60
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu		
65	70	75
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln		
85	90	95
Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp		
100	105	110
Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser		
115	120	125
Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala		
130	135	140
Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu		
145	150	155
Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln		
165	170	175
Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro		
180	185	190
Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln		
195	200	205
Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala		
210	215	220
Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe		
225	230	235
Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu		
245	250	255
Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly		
260	265	270
Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu		
275	280	285
Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser		
290	295	300
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile		
305	310	315
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu		
325	330	335
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr		
340	345	350
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His		
355	360	365
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu		
370	375	380
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr		

385		390		395		400										
Leu	Leu	Cys	Ile	Ala	Tyr	Val	Phe	Glu	Val	Ser	Ala	Ser	Glu	His	Gly	
		405						410						415		
Ala	Gln	His	His	Ile	Tyr	Arg	Leu	Val	Lys	Glu						
		420						425								

<210> 28

<211> 1281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1284)

<400> 28

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1			5					10					15			
gcc	tct	ggg	ggc	agt	cag	gca	ctg	gac	aag	ccc	atc	gac	aat	gac	gca	96
Ala	Ser	Gly	Gly	Ser	Gln	Ala	Leu	Asp	Lys	Pro	Ile	Asp	Asn	Asp	Ala	
			20					25					30			
gag	ggc	gtg	tgg	agc	ccg	gat	att	gag	cag	agt	ttc	cag	gag	gcc	ctc	144
Glu	Gly	Val	Trp	Ser	Pro	Asp	Ile	Glu	Gln	Ser	Phe	Gln	Glu	Ala	Leu	
			35					40					45			
gcc	atc	tac	ccg	ccc	tgt	ggc	agg	cgc	aaa	atc	atc	ctg	tcg	gac	gag	192
Ala	Ile	Tyr	Pro	Pro	Cys	Gly	Arg	Arg	Lys	Ile	Ile	Leu	Ser	Asp	Glu	
			50				55					60				
ggc	aag	atg	tat	ggt	cgg	aac	gag	ctg	att	gcc	cgc	tac	atc	aag	ctc	240
Gly	Lys	Met	Tyr	Gly	Arg	Asn	Glu	Leu	Ile	Ala	Arg	Tyr	Ile	Lys	Leu	
65					70					75				80		
cgg	aca	ggg	aag	acc	cgc	acc	agg	aag	cag	gtc	tcc	agc	cac	atc	cag	288
Arg	Thr	Gly	Lys	Thr	Arg	Thr	Arg	Lys	Gln	Val	Ser	Ser	His	Ile	Gln	
					85				90				95			
gtg	ctg	gct	cgt	cgc	aaa	gct	cgc	gag	atc	cag	gcc	aag	cta	aag	gac	336
Val	Leu	Ala	Arg	Arg	Lys	Ala	Arg	Glu	Ile	Gln	Ala	Lys	Leu	Lys	Asp	
			100					105				110				
cag	gca	gct	aag	gac	aag	gcc	ctg	cag	agc	atg	gct	gcc	atg	tcg	tct	384
Gln	Ala	Ala	Lys	Asp	Lys	Ala	Leu	Gln	Ser	Met	Ala	Ala	Met	Ser	Ser	
			115				120					125				
gca	cag	atc	atc	tcc	gcc	acg	gcc	ttc	cac	agt	agc	atg	gcc	ctc	gcc	432
Ala	Gln	Ile	Ile	Ser	Ala	Thr	Ala	Phe	His	Ser	Ser	Met	Ala	Leu	Ala	
			130				135					140				
cgg	ggc	ccc	ggc	cgc	cca	gca	gtc	tca	ggg	ttt	tgg	caa	gga	gct	ttg	480
Arg	Gly	Pro	Gly	Arg	Pro	Ala	Val	Ser	Gly	Phe	Trp	Gln	Gly	Ala	Leu	

145	150	155	160	
cca ggc caa gcc gga acg tcc cat gat gtg aag cct ttc tct cag caa				528
Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln				
	165	170	175	
acc tat gct gtc cag cct ccg ctg cct ctg cca ggg ttt gag tct cct				576
Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro				
	180	185	190	
gca ggg ccc gcc cca tcg ccc tct gcg ccc ccg gca ccc cca tgg cag				624
Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln				
	195	200	205	
ggc cgc agc gtg gcc agc tcc aag ctc tgg atg ttg gag ttc tct gcc				672
Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala				
	210	215	220	
ttc ctg gag cag cag cag gac ccg gac acg tac aac aag cac ctg ttc				720
Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe				
	225	230	235	240
gtg cac att ggc cag tcc agc cca agc tac agc gac ccc tac ctc gaa				768
Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu				
	245	250	255	
gcc gtg gac atc cgc caa atc tat gac aaa ttc ccg gag aaa aag ggt				816
Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly				
	260	265	270	
gga ctc aag gat ctc ttc gaa cgg gga ccc tcc aat gcc ttt ttt ctt				864
Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu				
	275	280	285	
gtg aag ttc tgg gca gac ctc aac acc aac atc gag gat gaa ggc agc				912
Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser				
	290	295	300	
tcc ttc tat ggg gtc tcc agc cag tat gag agc ccc gag aac atg atc				960
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile				
	305	310	315	320
atc acc tgc tcc acg aag gtc tgc tct ttc ggc aag cag gtg gtg gag				1008
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu				
	325	330	335	
aaa gtt gag aca gag tat gct cgc tat gag aat gga cac tac tct tac				1056
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr				
	340	345	350	
cgc atc cac cgg tcc ccg ctc tgt gag tac atg atc aac ttc atc cac				1104
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His				
	355	360	365	
aag ctc aag cac ctc cct gag aag tac atg atg aac agc gtg ctg gag				1152
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu				

370	375	380	
aac ttc acc atc ctg cag gtg gtc acc aac aga gac aca cag gag acc			1200
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr			
385	390	395	400
ttg ctg tgc att gcc tat gtc ttt gag gtg tca gcc agt gag cac ggg			1248
Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly			
	405	410	415
gct cag cac cac atc tac agg ctg gtg aaa gaa			1281
Ala Gln His His Ile Tyr Arg Leu Val Lys Glu			
	420	425	

<210> 29
 <211> 435
 <212> PRT
 <213> Homo sapiens
 <400> 29

Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg			
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Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu			
	20	25	30
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala			
	35	40	45
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly			
	50	55	60
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg			
	65	70	75
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val			
	85	90	95
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met			
	100	105	110
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser			
	115	120	125
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe			
	130	135	140
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg			
	145	150	155
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln			
	165	170	175
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu			
	180	185	190
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala			
	195	200	205
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg			

210	215	220	
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro			
225	230	235	240
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro			
	245	250	255
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr			
	260	265	270
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys			
	275	280	285
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn			
	290	295	300
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln			
305	310	315	320
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys			
	325	330	335
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg			
	340	345	350
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys			
	355	360	365
Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys			
	370	375	380
Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val			
385	390	395	400
Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe			
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Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu			
	420	425	430
Val Lys Asp			
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Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg			
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gag gat ggg ccc gag ggc ctg gac aag ggg ctg gac aac gat gcg gag	96		
Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu			
20 25 30			

ggc gtg tgg agc ccg gac atc gag cag agc ttc cag gag gcc ctg gcc	144
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala	
35 40 45	
atc tac ccg ccc tgc ggc cgg cgg aag atc atc ctg tca gac gag ggc	192
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly	
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aag atg tac ggc cga aat gag ttg att gca cgc tat att aaa ctg agg	240
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg	
65 70 75 80	
acg ggg aag act cgg acg aga aaa cag gtg tcc agc cac ata cag gtt	288
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val	
85 90 95	
cta gct cgg aag aag gtg cgg gag tac cag gtt ggc atc aag gcc atg	336
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met	
100 105 110	
aac ctg gac cag gtc tcc aag gac aaa gcc ctt cag agc atg gcg tcc	384
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser	
115 120 125	
atg tcc tct gcc cag atc gtc tct gcc agt gtc ctg cag aac aag ttc	432
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe	
130 135 140	
agc cca cct tcc cct ctg ccc cag gcc gtc ttc tcc act tcc tcg cgg	480
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg	
145 150 155 160	
ttc tgg agc agc ccc cct ctc ctg gga cag cag cct gga ccc tct cag	528
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln	
165 170 175	
gac atc aag ccc ttt gca cag cca gcc tac ccc atc cag ccg ccc ctg	576
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu	
180 185 190	
ccg ccg acg ctc agc agt tat gag ccc ctg gcc ccg ctc ccc tca gct	624
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala	
195 200 205	
gct gcc tct gtg cct gtg tgg cag gac cgt acc att gcc tcc tcc cgg	672
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg	
210 215 220	
ctg cgg ctc ctg gag tat tca gcc ttc atg gag gtg cag cga gac cct	720
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro	
225 230 235 240	
gac acg tac agc aaa cac ctg ttt gtg cac atc ggc cag acg aac ccc	768
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro	
245 250 255	

gcc ttc tca gac cca ccc ctg gag gca gta gat gtg cgc cag atc tat	816
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr	
260 265 270	
gac aaa ttc ccc gag aaa aag gga gga ttg aag gag ctc tat gag aag	864
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys	
275 280 285	
ggg ccc cct aat gcc ttc ttc ctt gtc aag ttc tgg gcc gac ctc aac	912
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn	
290 295 300	
agc acc atc cag gag ggc ccg gga gcc ttc tat ggg gtc agc tct cag	960
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln	
305 310 315 320	
tac agc tct gct gat agc atg acc atc agc gtc tcc acc aag gtg tgc	1008
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys	
325 330 335	
tcc ttt ggc aaa cag gtg gta gag aag gtg gag act gag tat gcc agg	1056
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg	
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ctg gag aac ggg cgc ttt gtg tac cgt atc cac cgc tcg ccc atg tgc	1104
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys	
355 360 365	
gag tac atg atc aac ttc atc cac aag ctg aag cac ctg ccc gag aag	1152
Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys	
370 375 380	
tac atg atg aac agc gtg ctg gag aac ttc acc atc ctg cag gtg gtc	1200
Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val	
385 390 395 400	
acg agc cgg gac tcc cag gag acc ttg ctt gtc att gct ttt gtc ttc	1248
Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe	
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gaa gtc tcc acc agt gag cac ggg gcc cag cac cat gtc tac aag ctc	1296
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gtc aaa gac	1305
Val Lys Asp	
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Pro Gln Gly	Trp Arg Leu Val Gln Arg	Gly Asp Pro Ala Ala	Phe Arg
35	40	45	
Ala Leu Val	Ala Gln Cys Leu Val Cys Val	Pro Trp Asp Ala Arg	Pro
50	55	60	
Pro Pro Ala	Ala Pro Ser Phe Arg Gln Val	Ser Cys Leu Lys Glu	Leu
65	70	75	80
Val Ala Arg	Val Leu Gln Arg Leu Cys Glu Arg	Gly Ala Lys Asn	Val
85	90	95	
Leu Ala Phe	Gly Phe Ala Leu Leu Asp Gly	Ala Arg Gly Gly	Pro Pro
100	105	110	
Glu Ala Phe	Thr Thr Ser Val Arg Ser Tyr	Leu Pro Asn Thr	Val Thr
115	120	125	
Asp Ala Leu	Arg Gly Ser Gly Ala Trp Gly	Leu Leu Leu Arg	Arg Val
130	135	140	
Gly Asp Asp	Val Leu Val His Leu Leu Ala	Arg Cys Ala Leu	Phe Val
145	150	155	160
Leu Val Ala	Pro Ser Cys Ala Tyr Gln Val	Cys Gly Pro Pro	Leu Tyr
165	170	175	
Gln Leu Gly	Ala Ala Thr Gln Ala Arg Pro	Pro Pro His Ala	Ser Gly
180	185	190	
Pro Arg Arg	Arg Leu Gly Cys Glu Arg Ala	Trp Asn His Ser	Val Arg
195	200	205	
Glu Ala Gly	Val Pro Leu Gly Leu Pro Ala	Pro Gly Ala Arg	Arg Arg
210	215	220	
Gly Gly Ser	Ala Ser Arg Ser Leu Pro Leu	Pro Lys Arg Pro	Arg Arg
225	230	235	240
Gly Ala Ala	Pro Glu Pro Glu Arg Thr Pro	Val Gly Gln Gly	Ser Trp
245	250	255	
Ala His Pro	Gly Arg Thr Arg Gly Pro Ser	Asp Arg Gly Phe	Cys Val
260	265	270	
Val Ser Pro	Ala Arg Pro Ala Glu Glu Ala	Thr Ser Leu Glu	Gly Ala
275	280	285	
Leu Ser Gly	Thr Arg His Ser His Pro Ser	Val Gly Arg Gln	His His
290	295	300	
Ala Gly Pro	Pro Ser Thr Ser Arg Pro Pro	Arg Pro Trp Asp	Thr Pro
305	310	315	320
Cys Pro Pro	Val Tyr Ala Glu Thr Lys His	Phe Leu Tyr Ser	Ser Gly
325	330	335	
Asp Lys Glu	Gln Leu Arg Pro Ser Phe Leu	Leu Ser Ser Leu	Arg Pro

340	345	350
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser		
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Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln		
370	375	380
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His		
385	390	395
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg		
405	410	415
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln		
420	425	430
Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu		
435	440	445
Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe		
450	455	460
Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser		
465	470	475
Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser		
485	490	495
Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met		
500	505	510
Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys		
515	520	525
Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe		
530	535	540
Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe		
545	550	555
Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr		
565	570	575
Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His		
580	585	590
Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln		
595	600	605
His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile		
610	615	620
Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val		
625	630	635
Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser		
645	650	655
Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg		
660	665	670
Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg		

675	680	685
Ala Trp Arg Thr Phe Val	Leu Arg Val Arg Ala	Gln Asp Pro Pro Pro
690	695	700
Glu Leu Tyr Phe Val Lys Val	Asp Val Thr Gly Ala Tyr	Asp Thr Ile
705	710	715
Pro Gln Asp Arg Leu Thr	Glu Val Ile Ala Ser Ile	Ile Lys Pro Gln
725	730	735
Asn Thr Tyr Cys Val Arg	Arg Tyr Ala Val Val	Gln Lys Ala Ala His
740	745	750
Gly His Val Arg Lys Ala Phe	Lys Ser His Val Ser Thr	Leu Thr Asp
755	760	765
Leu Gln Pro Tyr Met Arg	Gln Phe Val Ala His	Leu Gln Glu Thr Ser
770	775	780
Pro Leu Arg Asp Ala Val	Val Ile Glu Gln Ser Ser	Ser Leu Asn Glu
785	790	795
Ala Ser Ser Gly Leu Phe	Asp Val Phe Leu Arg Phe	Met Cys His His
805	810	815
Ala Val Arg Ile Arg Gly	Lys Ser Tyr Val Gln Cys	Gln Gly Ile Pro
820	825	830
Gln Gly Ser Ile Leu Ser	Thr Leu Leu Cys Ser Leu	Cys Tyr Gly Asp
835	840	845
Met Glu Asn Lys Leu Phe	Ala Gly Ile Arg Arg Asp	Gly Leu Leu Leu
850	855	860
Arg Leu Val Asp Asp Phe	Leu Leu Val Thr Pro His	Leu Thr His Ala
865	870	875
Lys Thr Phe Leu Arg Thr	Leu Val Arg Gly Val Pro	Glu Tyr Gly Cys
885	890	895
Val Val Asn Leu Arg Lys	Thr Val Val Asn Phe Pro	Val Glu Asp Glu
900	905	910
Ala Leu Gly Gly Thr Ala	Phe Val Gln Met Pro Ala	His Gly Leu Phe
915	920	925
Pro Trp Cys Gly Leu Leu	Leu Asp Thr Arg Thr Leu	Glu Val Gln Ser
930	935	940
Asp Tyr Ser Ser Tyr Ala	Arg Thr Ser Ile Arg Ala	Ser Leu Thr Phe
945	950	955
Asn Arg Gly Phe Lys Ala	Gly Arg Asn Met Arg Arg	Lys Leu Phe Gly
965	970	975
Val Leu Arg Leu Lys Cys	His Ser Leu Phe Leu Asp	Leu Gln Val Asn
980	985	990
Ser Leu Gln Thr Val Cys	Thr Asn Ile Tyr Lys Ile	Leu Leu Leu Gln
995	1000	1005
Ala Tyr Arg Phe His Ala	Cys Val Leu Gln Leu Pro	Phe His Gln Gln

1010	1015	1020
Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala		
1025	1030	1035
Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu		1040
	1045	1050
Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp		1055
	1060	1065
Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr		1070
	1075	1080
Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser		1085
	1090	1095
Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn		1100
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Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp		1120
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cac tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg	96
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly	
20 25 30	
ccc cag ggc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc	144
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg	
35 40 45	
gcg ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg	192
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro	
50 55 60	
ccc ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg	240
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu	
65 70 75 80	
gtg gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg	288
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val	
85 90 95	
ctg gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc	336

Leu	Ala	Phe	Gly	Phe	Ala	Leu	Leu	Asp	Gly	Ala	Arg	Gly	Gly	Pro	Pro		
			100					105					110				
gag	gcc	ttc	acc	acc	agc	gtg	cgc	agc	tac	ctg	ccc	aac	acg	gtg	acc	384	
Glu	Ala	Phe	Thr	Thr	Ser	Val	Arg	Ser	Tyr	Leu	Pro	Asn	Thr	Val	Thr		
			115				120					125					
gac	gca	ctg	cgg	ggg	agc	ggg	gcg	tgg	ggg	ctg	ctg	ctg	cgc	cgc	gtg	432	
Asp	Ala	Leu	Arg	Gly	Ser	Gly	Ala	Trp	Gly	Leu	Leu	Leu	Arg	Arg	Val		
			130				135					140					
ggc	gac	gac	gtg	ctg	gtt	cac	ctg	ctg	gca	cgc	tgc	gcg	ctc	ttt	gtg	480	
Gly	Asp	Asp	Val	Leu	Val	His	Leu	Leu	Ala	Arg	Cys	Ala	Leu	Phe	Val		
			145			150				155				160			
ctg	gtg	gct	ccc	agc	tgc	gcc	tac	cag	gtg	tgc	ggg	ccg	ccg	ctg	tac	528	
Leu	Val	Ala	Pro	Ser	Cys	Ala	Tyr	Gln	Val	Cys	Gly	Pro	Pro	Leu	Tyr		
			165					170					175				
cag	ctc	ggc	gct	gcc	act	cag	gcc	cgg	ccc	ccg	cca	cac	gct	agt	gga	576	
Gln	Leu	Gly	Ala	Ala	Thr	Gln	Ala	Arg	Pro	Pro	Pro	His	Ala	Ser	Gly		
			180				185					190					
ccc	cga	agg	cgt	ctg	gga	tgc	gaa	cgg	gcc	tgg	aac	cat	agc	gtc	agg	624	
Pro	Arg	Arg	Arg	Leu	Gly	Cys	Glu	Arg	Ala	Trp	Asn	His	Ser	Val	Arg		
			195				200				205						
gag	gcc	ggg	gtc	ccc	ctg	ggc	ctg	cca	gcc	ccg	ggt	gcg	agg	agg	cgc	672	
Glu	Ala	Gly	Val	Pro	Leu	Gly	Leu	Pro	Ala	Pro	Gly	Ala	Arg	Arg	Arg		
			210				215				220						
ggg	ggc	agt	gcc	agc	cga	agt	ctg	ccg	ttg	ccc	aag	agg	ccc	agg	cgt	720	
Gly	Gly	Ser	Ala	Ser	Arg	Ser	Leu	Pro	Leu	Pro	Lys	Arg	Pro	Arg	Arg		
			225			230			235			240					
ggc	gct	gcc	cct	gag	ccg	gag	cgg	acg	ccc	gtt	ggg	cag	ggg	tcc	tgg	768	
Gly	Ala	Ala	Pro	Glu	Pro	Glu	Arg	Thr	Pro	Val	Gly	Gln	Gly	Ser	Trp		
			245				250				255						
gcc	cac	ccg	ggc	agg	acg	cgt	gga	ccg	agt	gac	cgt	ggt	ttc	tgt	gtg	816	
Ala	His	Pro	Gly	Arg	Thr	Arg	Gly	Pro	Ser	Asp	Arg	Gly	Phe	Cys	Val		
			260				265					270					
gtg	tca	cct	gcc	aga	ccc	gcc	gaa	gaa	gcc	acc	tct	ttg	gag	ggt	gcg	864	
Val	Ser	Pro	Ala	Arg	Pro	Ala	Glu	Glu	Ala	Thr	Ser	Leu	Glu	Gly	Ala		
			275				280					285					
ctc	tct	ggc	acg	cgc	cac	tcc	cac	cca	tcc	gtg	ggc	cgc	cag	cac	cac	912	
Leu	Ser	Gly	Thr	Arg	His	Ser	His	Pro	Ser	Val	Gly	Arg	Gln	His	His		
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gcg	ggc	ccc	cca	tcc	aca	tcg	cgg	cca	cca	cgt	ccc	tgg	gac	acg	cct	960	
Ala	Gly	Pro	Pro	Ser	Thr	Ser	Arg	Pro	Pro	Arg	Pro	Trp	Asp	Thr	Pro		
			305			310				315				320			
tgt	ccc	ccg	gtg	tac	gcc	gag	acc	aag	cac	ttc	ctc	tac	tcc	tca	ggc	1008	

Leu	His	Trp	Leu	Met	Ser	Val	Tyr	Val	Val	Glu	Leu	Leu	Arg	Ser	Phe		
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ttt	tat	gtc	acg	gag	acc	acg	ttt	caa	aag	aac	agg	ctc	ttt	ttc	tac	1728	
Phe	Tyr	Val	Thr	Glu	Thr	Thr	Phe	Gln	Lys	Asn	Arg	Leu	Phe	Phe	Tyr		
				565						570					575		
cgg	aag	agt	gtc	tgg	agc	aag	ttg	caa	agc	att	gga	atc	aga	cag	cac	1776	
Arg	Lys	Ser	Val	Trp	Ser	Lys	Leu	Gln	Ser	Ile	Gly	Ile	Arg	Gln	His		
				580						585					590		
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Leu	Lys	Arg	Val	Gln	Leu	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Val	Arg	Gln		
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cat	cgg	gaa	gcc	agg	ccc	gcc	ctg	ctg	acg	tcc	aga	ctc	cgc	ttc	atc	1872	
His	Arg	Glu	Ala	Arg	Pro	Ala	Leu	Leu	Thr	Ser	Arg	Leu	Arg	Phe	Ile		
				610						615					620		
ccc	aag	cct	gac	ggg	ctg	cgg	ccg	att	gtg	aac	atg	gac	tac	gtc	gtg	1920	
Pro	Lys	Pro	Asp	Gly	Leu	Arg	Pro	Ile	Val	Asn	Met	Asp	Tyr	Val	Val		
				625						630					640		
gga	gcc	aga	acg	ttc	cgc	aga	gaa	aag	agg	gcc	gag	cgt	ctc	acc	tcg	1968	
Gly	Ala	Arg	Thr	Phe	Arg	Arg	Glu	Lys	Arg	Ala	Glu	Arg	Leu	Thr	Ser		
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agg	gtg	aag	gca	ctg	ttc	agc	gtg	ctc	aac	tac	gag	cgg	gcg	cgg	cgc	2016	
Arg	Val	Lys	Ala	Leu	Phe	Ser	Val	Leu	Asn	Tyr	Glu	Arg	Ala	Arg	Arg		
				660						665					670		
ccc	ggc	ctc	ctg	ggc	gcc	tct	gtg	ctg	ggc	ctg	gac	gat	atc	cac	agg	2064	
Pro	Gly	Leu	Leu	Gly	Ala	Ser	Val	Leu	Gly	Leu	Asp	Asp	Ile	His	Arg		
				675						680					685		
gcc	tgg	cgc	acc	ttc	gtg	ctg	cgt	gtg	cgg	gcc	cag	gac	ccg	ccg	cct	2112	
Ala	Trp	Arg	Thr	Phe	Val	Leu	Arg	Val	Arg	Ala	Gln	Asp	Pro	Pro	Pro		
				690						695					700		
gag	ctg	tac	ttt	gtc	aag	gtg	gat	gtg	acg	ggc	gcg	tac	gac	acc	atc	2160	
Glu	Leu	Tyr	Phe	Val	Lys	Val	Asp	Val	Thr	Gly	Ala	Tyr	Asp	Thr	Ile		
				705						710					715		
ccc	cag	gac	agg	ctc	acg	gag	gtc	atc	gcc	agc	atc	atc	aaa	ccc	cag	2208	
Pro	Gln	Asp	Arg	Leu	Thr	Glu	Val	Ile	Ala	Ser	Ile	Ile	Lys	Pro	Gln		
				725						730					735		
aac	acg	tac	tgc	gtg	cgt	cgg	tat	gcc	gtg	gtc	cag	aag	gcc	gcc	cat	2256	
Asn	Thr	Tyr	Cys	Val	Arg	Arg	Tyr	Ala	Val	Val	Gln	Lys	Ala				

Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser	
770 775 780	
ccg ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag	2400
Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu	
785 790 795 800	
gcc agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac	2448
Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His	
805 810 815	
gcc gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg	2496
Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro	
820 825 830	
cag ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac	2544
Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp	
835 840 845	
atg gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg	2592
Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu	
850 855 860	
cgt ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg	2640
Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala	
865 870 875 880	
aaa acc ttc ctc agg acc ctg gtc cga ggt gtc cct gag tat ggc tgc	2688
Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys	
885 890 895	
gtg gtg aac ttg cgg aag aca gtg gtg aac ttc cct gta gaa gac gag	2736
Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu	
900 905 910	
gcc ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc	2784
Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe	
915 920 925	
ccc tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc	2832
Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser	
930 935 940	
gac tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc	2880
Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe	
945 950 955 960	
aac cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg	2928
Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly	
965 970 975	
gtc ttg cgg ctg aag tgt cac agc ctg ttt ctg gat ttg cag gtg aac	2976
Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn	
980 985 990	
agc ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag	3024

Ser	Leu	Gln	Thr	Val	Cys	Thr	Asn	Ile	Tyr	Lys	Ile	Leu	Leu	Leu	Gln	
	995						1000					1005				
gcg	tac	agg	ttt	cac	gca	tgt	gtg	ctg	cag	ctc	cca	ttt	cat	cag	caa	3072
Ala	Tyr	Arg	Phe	His	Ala	Cys	Val	Leu	Gln	Leu	Pro	Phe	His	Gln	Gln	
	1010						1015					1020				
ggt	tgg	aag	aac	ccc	aca	ttt	ttc	ctg	cgc	gtc	atc	tct	gac	acg	gcc	3120
Val	Trp	Lys	Asn	Pro	Thr	Phe	Phe	Leu	Arg	Val	Ile	Ser	Asp	Thr	Ala	
	1025						1030					1035				1040
tcc	ctc	tgc	tac	tcc	atc	ctg	aaa	gcc	aag	aac	gca	ggg	atg	tcg	ctg	3168
Ser	Leu	Cys	Tyr	Ser	Ile	Leu	Lys	Ala	Lys	Asn	Ala	Gly	Met	Ser	Leu	
			1045						1050					1055		
ggg	gcc	aag	ggc	gcc	gcc	ggc	cct	ctg	ccc	tcc	gag	gcc	gtg	cag	tgg	3216
Gly	Ala	Lys	Gly	Ala	Ala	Gly	Pro	Leu	Pro	Ser	Glu	Ala	Val	Gln	Trp	
			1060						1065					1070		
ctg	tgc	cac	caa	gca	ttc	ctg	ctc	aag	ctg	act	cga	cac	cgt	gtc	acc	3264
Leu	Cys	His	Gln	Ala	Phe	Leu	Leu	Lys	Leu	Thr	Arg	His	Arg	Val	Thr	
			1075						1080					1085		
tac	gtg	cca	ctc	ctg	ggg	tca	ctc	agg	aca	gcc	cag	acg	cag	ctg	agt	3312
Tyr	Val	Pro	Leu	Leu	Gly	Ser	Leu	Arg	Thr	Ala	Gln	Thr	Gln	Leu	Ser	
		1090					1095					1100				
cgg	aag	ctc	ccg	ggg	acg	acg	ctg	act	gcc	ctg	gag	gcc	gca	gcc	aac	3360
Arg	Lys	Leu	Pro	Gly	Thr	Thr	Leu	Thr	Ala	Leu	Glu	Ala	Ala	Ala	Asn	
		1105					1110					1115				1120
ccg	gca	ctg	ccc	tca	gac	ttc	aag	acc	atc	ctg	gac					3396
Pro	Ala	Leu	Pro	Ser	Asp	Phe	Lys	Thr	Ile	Leu	Asp					
			1125						1130							

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 33

ttggttcca ggccataatt g

21

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 34

aagagggcag atctatcgga 20
 <210> 35
 <211> 20
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 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 35
 atggatctcc tgaaggtgct 20
 <210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 36
 aagagggcag atctatcgga 20
 <210> 37
 <211> 23
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 37
 ggaagagtga gcggccatca agg 23
 <210> 38
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 38
 ctgctggaga ggttattcct cg 22
 <210> 39
 <211> 24
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 39
 gccaacacca acctgtccaa gttc 24
 <210> 40

<211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 40
 tgcaaaggct ccaggtctga gggc 24
 <210> 41
 <211> 19
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 41
 ctctctctcc tcaggacaa 19
 <210> 42
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 42
 tggagcaaaa cagaatggct gg 22
 <210> 43
 <211> 24
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 43
 ctgagatgtc tctctctctc ttag 24
 <210> 44
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 44
 acaatgactg atgagagatg 20
 <210> 45
 <211> 18
 <212> DNA

<213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 45
 cagacctgaa ggagacct 18
 <210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 46
 gtcagcgtaa acagttgc 18
 <210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 47
 gccaaagaagc ggatagaagg 20
 <210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 48
 ctgtggttca gggctcagtc 20
 <210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 49
 cagtggagct ggacaaagcc 20
 <210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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<223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 50
 tagcgacggt tctggaacca 20
 <210> 51
 <211> 20
 <212> DNA
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 51
 ctgtcatctc actatgggca 20
 <210> 52
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 52
 ccaagtccga gcaggaattt 20
 <210> 53
 <211> 20
 <212> DNA
 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 53
 aagacgtcaa gccctttgtg 20
 <210> 54
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 54
 aaaggagcac actttggtgg 20
 <210> 55
 <211> 20
 <212> DNA
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 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 55

agcaagaata cgatgccatc 20

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223>Description of Artificial Sequence: artificially synthesized primer sequence

<400> 56

gaaggggtgg tggtacggtc 20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 57

tgggaatggc tatgtcagtg 20

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 58

ctggtaatct gtgtttagg 20

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 59

caagggcctc tccaaacttg 20

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 60

gccccagaga cagcattcca 20

<210> 61

<211> 268

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser
1 5 10 15

Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys
20 25 30

Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala
35 40 45

Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
50 55 60

Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
65 70 75 80

Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
85 90 95

Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
100 105 110

Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
115 120 125

Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
130 135 140

Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
145 150 155 160

Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
165 170 175

Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
180 185 190

Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro

195	200	205	
Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala			
210	215	220	
Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser			
225	230	235	240
Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro			
245	250	255	
Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys			
260	265		
<210> 62			
<211> 804			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<223> (1)..(807)			
<400> 62			
atg gcc cag ccc ctg tgc ccg ccg ctc tcc gag tcc tgg atg ctc tct	48		
Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser			
1 5 10 15			
gcg gcc tgg ggc cca act cgg cgg ccg ccg ccc tcc gac aag gac tgc	96		
Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys			
20 25 30			
ggc cgc tcc ctc gtc tcg tcc cca gac tca tgg ggc agc acc cca gcc	144		
Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala			
35 40 45			
gac agc ccc gtg gcg agc ccc gcg cgg cca ggc acc ctc cgg gac ccc	192		
Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro			
50 55 60			
cgc gcc ccc tcc gta ggt agg cgc ggc gcg cgc agc agc cgc ctg ggc	240		
Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly			
65 70 75 80			
agc ggg cag agg cag agc gcc agt gag cgg gag aaa ctg cgc atg cgc	288		

Ser	Gly	Gln	Arg	Gln	Ser	Ala	Ser	Glu	Arg	Glu	Lys	Leu	Arg	Met	Arg		
				85					90					95			
acg	ctg	gcc	cgc	gcc	ctg	cac	gag	ctg	cgc	cgc	ttt	cta	ccg	ccg	tcc	336	
Thr	Leu	Ala	Arg	Ala	Leu	His	Glu	Leu	Arg	Arg	Phe	Leu	Pro	Pro	Ser		
			100					105					110				
gtg	gcg	ccc	gcg	ggc	cag	agc	ctg	acc	aag	atc	gag	acg	ctg	cgc	ctg	384	
Val	Ala	Pro	Ala	Gly	Gln	Ser	Leu	Thr	Lys	Ile	Glu	Thr	Leu	Arg	Leu		
			115					120					125				
gct	atc	cgc	tat	atc	ggc	cac	ctg	tgc	gcc	gtg	cta	ggc	ctc	agc	gag	432	
Ala	Ile	Arg	Tyr	Ile	Gly	His	Leu	Ser	Ala	Val	Leu	Gly	Leu	Ser	Glu		
			130			135					140						
gag	agt	ctc	cag	cgc	cgg	tgc	cgg	cag	cgc	ggt	gac	gcg	ggg	tcc	cct	480	
Glu	Ser	Leu	Gln	Arg	Arg	Cys	Arg	Gln	Arg	Gly	Asp	Ala	Gly	Ser	Pro		
			145			150				155					160		
cgg	ggc	tgc	ccg	ctg	tgc	ccc	gac	gac	tgc	ccc	gcg	cag	atg	cag	aca	528	
Arg	Gly	Cys	Pro	Leu	Cys	Pro	Asp	Asp	Cys	Pro	Ala	Gln	Met	Gln	Thr		
			165						170					175			
cgg	acg	cag	gct	gag	ggg	cag	ggg	cag	ggg	cgc	ggg	ctg	ggc	ctg	gta	576	
Arg	Thr	Gln	Ala	Glu	Gly	Gln	Gly	Gln	Gly	Arg	Gly	Leu	Gly	Leu	Val		
			180					185					190				
tcc	gcc	gtc	cgc	gcc	ggg	gcg	tcc	tgg	gga	tcc	ccg	cct	gcc	tgc	ccc	624	
Ser	Ala	Val	Arg	Ala	Gly	Ala	Ser	Trp	Gly	Ser	Pro	Pro	Ala	Cys	Pro		
			195					200					205				
gga	gcc	cga	gct	gca	ccc	gag	ccg	cgc	gac	ccg	cct	gcg	ctg	ttc	gcc	672	
Gly	Ala	Arg	Ala	Ala	Pro	Glu	Pro	Arg	Asp	Pro	Pro	Ala	Leu	Phe	Ala		
			210					215					220				
gag	gcg	gcg	tgc	cct	gaa	ggg	cag	gcg	atg	gag	cca	agc	cca	ccg	tcc	720	
Glu	Ala	Ala	Cys	Pro	Glu	Gly	Gln	Ala	Met	Glu	Pro	Ser	Pro	Pro	Ser		
			225					230					235		240		
ccg	ctc	ctt	ccg	ggc	gac	gtg	ctg	gct	ctg	ttg	gag	acc	tgg	atg	ccc	768	
Pro	Leu	Leu	Pro	Gly	Asp	Val	Leu	Ala	Leu	Leu	Glu	Thr	Trp	Met	Pro		
			245						250					255			

ctc tcg cct ctg gag tgg ctg cct gag gag ccc aag
 Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys

804

260

265

<210> 63

<211> 215

<212> PRT

<213> Homo sapiens

<400> 63

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45

Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60

Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80

Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
 85 90 95

Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
 100 105 110

Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
 115 120 125

Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
 130 135 140

Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
 145 150 155 160

Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
 165 170 175

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu

180	185	190	
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg			
195	200	205	
Thr Trp Ala Pro Glu Pro Arg			
210			
<210> 64			
<211> 645			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<223> (1)..(648)			
<400> 64			
atg ggc agc ccc cgc tcc gcg ctg agc tgc ctg ctg ttg cac ttg ctg	48		
Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu			
1 5 10 15			
gtc ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt	96		
Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe			
20 25 30			
aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc	144		
Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg			
35 40 45			
cgc ctc atc cgg acc tac caa ctc tac agc cgc acc agc ggg aag cac	192		
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His			
50 55 60			
gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gag gac ggc	240		
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly			
65 70 75 80			
gac ccc ttc gca aag ctc atc gtg gag acg gac acc ttt gga agc aga	288		
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg			
85 90 95			
gtt cga gtc cga gga gcc gag acg ggc ctc tac atc tgc atg aac aag	336		
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys			

100	105	110	
aag ggg aag ctg atc gcc aag agc aac ggc aaa ggc aag gac tgc gtc			384
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val			
115	120	125	
ttc acg gag att gtg ctg gag aac aac tac aca gcg ctg cag aat gcc			432
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala			
130	135	140	
aag tac gag ggc tgg tac atg gcc ttc acc cgc aag ggc cgg ccc cgc			480
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg			
145	150	155	160
aag ggc tcc aag acg cgg cag cac cag cgt gag gtc cac ttc atg aag			528
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys			
165	170	175	
cgg ctg ccc cgg ggc cac cac acc acc gag cag agc ctg cgc ttc gag			576
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu			
180	185	190	
ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg			624
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg			
195	200	205	
act tgg gcc ccg gaa ccc cga			645
Thr Trp Ala Pro Glu Pro Arg			
210	215		
<210> 65			
<211> 212			
<212> PRT			
<213> Homo sapiens			
<400> 65			
Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln			
1	5	10	15
Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly			
20	25	30	
Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg			
35	40	45	

Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val
 50 55 60

Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val
 65 70 75 80

Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn
 85 90 95

Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala
 100 105 110

Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu
 115 120 125

Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys
 130 135 140

Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu
 145 150 155 160

Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
 165 170 175

Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

Arg Ala His Trp
 210

<210> 66

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1) .. (639)

<400> 66

atg gat tat ttg ctc atg att ttc tct ctg ctg ttt gtg gct tgc caa 48
 Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln

1	5	10	15	
gga gct cca gaa aca gca gtc tta ggc gct gag ctc agc gcg gtg ggt	96			
Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly				
20	25	30		
gag aac ggc ggg gag aaa ccc act ccc agt cca ccc tgg cgg ctc cgc	144			
Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg				
35	40	45		
cgg tcc aag cgc tgc tcc tgc tgc tcc ctg atg gat aaa gag tgt gtc	192			
Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val				
50	55	60		
tac ttc tgc cac ctg gac atc att tgg gtc aac act ccc gag cac gtt	240			
Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val				
65	70	75	80	
gtt ccg tat gga ctt gga agc cct agg tcc aag aga gcc ttg gag aat	288			
Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn				
85	90	95		
tta ctt ccc aca aag gca aca gac cgt gag aat aga tgc caa tgt gct	336			
Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala				
100	105	110		
agc caa aaa gac aag aag tgc tgg aat ttt tgc caa gca gga aaa gaa	384			
Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu				
115	120	125		
ctc agg gct gaa gac att atg gag aaa gac tgg aat aat cat aag aaa	432			
Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys				
130	135	140		
gga aaa gac tgt tcc aag ctt ggg aaa aag tgt att tat cag cag tta	480			
Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu				
145	150	155	160	
gtg aga gga aga aaa atc aga aga agt tca gag gaa cac cta aga caa	528			
Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln				
165	170	175		

acc agg tcg gag acc atg aga aac agc gtc aaa tca tct ttt cat gat 576
 Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

ccc aag ctg aaa ggc aag ccc tcc aga gag cgt tat gtg acc cac aac 624
 Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

cga gca cat tgg 636
 Arg Ala His Trp
 210

<210> 67

<211> 143

<212> PRT

<213> Homo sapiens

<400> 67

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
 85 90 95

Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
 100 105 110

Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
 115 120 125

Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 130 135 140

<210> 68

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(432)

<400> 68

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Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
1 5 10 15

ctc acc tcc gcg gtc gcc aaa aag aaa gat aag gtg aag aag ggc ggc 96
Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
20 25 30

ccg ggg agc gag tgc gct gag tgg gcc tgg ggg ccc tgc acc ccc agc 144
Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
35 40 45

agc aag gat tgc ggc gtg ggt ttc cgc gag ggc acc tgc ggg gcc cag 192
Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
50 55 60

acc cag cgc atc cgg tgc agg gtg ccc tgc aac tgg aag aag gag ttt 240
Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
65 70 75 80

gga gcc gac tgc aag tac aag ttt gag aac tgg ggt gcg tgt gat ggg 288
Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
85 90 95

ggc aca ggc acc aaa gtc cgc caa ggc acc ctg aag aag gcg cgc tac 336
Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
100 105 110

aat gct cag tgc cag gag acc atc cgc gtc acc aag ccc tgc acc ccc 384
Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
115 120 125

aag acc aaa gca aag gcc aaa gcc aag aaa ggg aag gga aag gac 429
Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp

130 135 140
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 <211> 408
 <212> PRT
 <213> Homo sapiens
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 Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
 1 5 10 15
 Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
 20 25 30
 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
 35 40 45
 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 50 55 60
 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 65 70 75 80
 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 85 90 95
 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
 100 105 110
 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
 115 120 125
 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
 130 135 140
 Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
 145 150 155 160
 Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
 165 170 175
 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
 180 185 190

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
195 200 205

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
210 215 220

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
225 230 235 240

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
245 250 255

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
260 265 270

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
275 280 285

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
305 310 315 320

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
325 330 335

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
340 345 350

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
355 360 365

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
370 375 380

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
385 390 395 400

Val Val Glu Gly Cys Gly Cys Arg
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<212> DNA

<213> Homo sapiens

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<221> CDS

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Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val	
1 5 10 15	

ctg cta gga ggc gcg agc cat gct agt ttg ata cct gag acg ggg aag	96
Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys	
20 25 30	

aaa aaa gtc gcc gag att cag ggc cac gcg gga gga cgc cgc tca ggg	144
Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly	
35 40 45	

cag agc cat gag ctc ctg cgg gac ttc gag gcg aca ctt ctg cag atg	192
Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met	
50 55 60	

ttt ggg ctg cgc cgc cgc ccg cag cct agc aag agt gcc gtc att ccg	240
Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro	
65 70 75 80	

gac tac atg cgg gat ctt tac cgg ctt cag tct ggg gag gag gag gaa	288
Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu	
85 90 95	

gag cag atc cac agc act ggt ctt gag tat cct gag cgc ccg gcc agc	336
Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser	
100 105 110	

cgg gcc aac acc gtg agg agc ttc cac cac gaa gaa cat ctg gag aac	384
Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn	
115 120 125	

atc cca ggg acc agt gaa aac tct gct ttt cgt ttc ctc ttt aac ctc	432
Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu	
130 135 140	

agc agc atc cct gag aac gag gcg atc tcc tct gca gag ctt cgg ctc	480
Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu	
145 150 155 160	
ttc cgg gag cag gtg gac cag ggc cct gat tgg gaa agg ggc ttc cac	528
Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His	
165 170 175	
cgt ata aac att tat gag gtt atg aag ccc cca gca gaa gtg gtg cct	576
Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro	
180 185 190	
ggg cac ctc atc aca cga cta ctg gac acg aga ctg gtc cac cac aat	624
Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn	
195 200 205	
gtg aca cgg tgg gaa act ttt gat gtg agc cct gcg gtc ctt cgc tgg	672
Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp	
210 215 220	
acc cgg gag aag cag cca aac tat ggg cta gcc att gag gtg act cac	720
Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His	
225 230 235 240	
ctc cat cag act cgg acc cac cag ggc cag cat gtc agg att agc cga	768
Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg	
245 250 255	
tcg tta cct caa ggg agt ggg aat tgg gcc cag ctc cgg ccc ctc ctg	816
Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu	
260 265 270	
gtc acc ttt ggc cat gat ggc cgg ggc cat gcc ttg acc cga cgc cgg	864
Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg	
275 280 285	
agg gcc aag cgt agc cct aag cat cac tca cag cgg gcc agg aag aag	912
Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys	
290 295 300	
aat aag aac tgc cgg cgc cac tcg ctc tat gtg gac ttc agc gat gtg	960
Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val	

305	310	315	320	
ggc tgg aat gac tgg att gtg gcc cca cca ggc tac cag gcc ttc tac				1008
Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr				
	325	330	335	
tgc cat ggg gac tgc ccc ttt cca ctg gct gac cac ctc aac tca acc				1056
Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr				
	340	345	350	
aac cat gcc att gtg cag acc ctg gtc aat tct gtc aat tcc agt atc				1104
Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile				
	355	360	365	
ccc aaa gcc tgt tgt gtg ccc act gaa ctg agt gcc atc tcc atg ctg				1152
Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu				
	370	375	380	
tac ctg gat gag tat gat aag gtg gta ctg aaa aat tat cag gag atg				1200
Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met				
	385	390	395	400
gta gta gag gga tgt ggg tgc cgc				1224
Val Val Glu Gly Cys Gly Cys Arg				
	405			
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tgcttacggg ggtgcgccct ctgc				24
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<400> 73

gaagcgcaac agggccatca cg

22

<210> 74

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<212> DNA

<213> Artificial Sequence

<400> 74

ccacgtcacg caggtcccgt tc

22

<210> 75

<211> 22

<212> DNA

<213> Artificial Sequence

<400> 75

gatcctgttc tctgcctctg ga

22

<210> 76

<211> 22

<212> DNA

<213> Artificial Sequence

<400> 76

tcattccactt tgtccaccg ag

22

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ttcctcgtct tggccttttg g

21

<210> 78

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<212> DNA

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gctggatctt cgtaggctcc g

21

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19

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gggtgctcag gtagtggtt

19

NY_MAIN 231957v1